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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/076,406

DATE: 03/04/2002

TIME: 15:50:57

Input Set : A:\219774US0XCIP.ST25.txt
 Output Set: N:\CRF3\03042002\J076406.raw

3 <110> APPLICANT: MOECKEL, Bettina
 4 BATHE, Brigitte
 5 HERMANN, Thomas
 6 PFEFFERLE, Walter
 7 BINDER, Michael
 9 <120> TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
 11 <130> FILE REFERENCE: 219774US0XCIP
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/076,406
 14 <141> CURRENT FILING DATE: 2002-02-19
 16 <150> PRIOR APPLICATION NUMBER: DE 10107229.5
 17 <151> PRIOR FILING DATE: 2001-02-16
 19 <150> PRIOR APPLICATION NUMBER: US 09/887052
 20 <151> PRIOR FILING DATE: 2001-06-25
 22 <160> NUMBER OF SEQ ID NOS: 12
 24 <170> SOFTWARE: PatentIn version 3.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 5099
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Corynebacterium glutamicum
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (702)..(4196)
 34 <223> OTHER INFORMATION:
 37 <400> SEQUENCE: 1
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 42 tcgacgcctc cctcgacgat gcagctgtct ctaagctgg tgcacaggcc gaaagcatcc 180
 44 ctgatggaga tgtgagcaaa atcgcaaata ccgttaggtat tgtgatcggt gcggtattgg 240
 46 ctctcggtgg cctggccggg tgggggggg cggtggaa gaaacgtcga gaagcttaac 300
 48 ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt tggttgctag 360
 50 ggtgcctcgt agaagggttc aagaagattt ctggaaaacg cggccgtcgt gttgggtgct 420
 52 aatagcacgc ggagcacccag atgaaaaatc tccccttac ttccgcgcgc gattggata 480
 54 ctctgagtgc ttgcgttggaa attcgact cttttcggtt cctgttagcgc caagacattt 540
 56 atcaagggtgg tttaaaaaaa ccgatttgac aaggtcattt agtgcstatct ggagtcgttc 600
 58 agggggatcg ggttcctcag cagaccaatt gctaaaaat accagcggtt ttgatctgca 660
 60 cttaatggcc ttgaccagcc aggtgcaatt acccgctgaa g gtg ctg gaa gga ccc 716
 61 Val Leu Glu Gly Pro
 62 1 5
 64 atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt 764
 65 Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly
 66 10 15 20
 68 gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg 812
 69 Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val

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70	25	30	35	
72	ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt			860
73	Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly			
74	40	45	50	
76	acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc			908
77	Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala			
78	55	60	65	
80	cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc			956
81	Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile			
82	70	75	80	85
84	cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc			1004
85	Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe			
86	90	95	100	
88	gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac			1052
89	Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn			
90	105	110	115	
92	tac gcg gcg cca ctg tat gtg acc ggc gag ttc gtc aac aac acc acc			1100
93	Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr			
94	120	125	130	
96	ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg			1148
97	Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met			
98	135	140	145	
100	acg gac aag gga acg ttc atc atc aac gga acc gca cgc gtt gtg gtc			1196
101	Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val			
102	150	155	160	165
104	agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat			1244
105	Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp			
106	170	175	180	
108	aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt			1292
109	Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg			
110	185	190	195	
112	ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt			1340
113	Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val			
114	200	205	210	
116	cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct			1388
117	Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala			
118	215	220	225	
120	ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa			1436
121	Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu			
122	230	235	240	245
124	atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag			1484
125	Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu			
126	250	255	260	
128	gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc			1532
129	Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr			
130	265	270	275	
132	cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag			1580
133	Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys			
134	280	285	290	

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136	cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc	1628
137	Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu	
138	295 300 305	
140	ggc ctt ggt ggc gac cac gat ggt ttg atg act ctt act gaa gag gac	1676
141	Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp	
142	310 315 320 325	
144	atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc	1724
145	Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg	
146	330 335 340	
148	gtc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac	1772
149	Val Met Thr Ser Pro Asn Gly Glu Ile Pro Val Glu Thr Asp Asp	
150	345 350 355	
152	atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc	1820
153	Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile	
154	360 365 370	
156	cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt	1868
157	Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg	
158	375 380 385	
160	gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg	1916
161	Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu	
162	390 395 400 405	
164	atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act	1964
165	Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr	
166	410 415 420	
168	tcc cag ctg tct cag ttc atg gac cag aac aac tcc ctg tct ggt ttg	2012
169	Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn Ser Leu Ser Gly Leu	
170	425 430 435	
172	act cac aag cgt cgt ctg gct ctg ggc ccg ggt ggt ctg tcc cgt	2060
173	Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg	
174	440 445 450	
176	gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc	2108
177	Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly	
178	455 460 465	
180	cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc	2156
181	Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile	
182	470 475 480 485	
184	ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag	2204
185	Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu	
186	490 495 500	
188	acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gag	2252
189	Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp	
190	505 510 515	
192	tac ctt acc gct gat gag gaa gac cgc ttc gtt gct gca cag gca aac	2300
193	Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val Val Ala Gln Ala Asn	
194	520 525 530	
196	acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348
197	Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val	
198	535 540 545	
200	cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396

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201	Arg	Leu	Lys	Asp	Gly	Asp	Ile	Ala	Met	Val	Gly	Arg	Asn	Ala	Val	Asp	
202	550			555					560						565		
204	tac	atg	gac	gtt	tcc	cct	cgt	cag	atg	gtt	tct	gtt	ggt	acc	gcg	atg	2444
205	Tyr	Met	Asp	Val	Ser	Pro	Arg	Gln	Met	Val	Ser	Val	Gly	Thr	Ala	Met	
206									570			575				580	
208	att	cca	ttc	ctg	gag	cac	gac	gat	gct	aac	cgt	gca	ctg	atg	ggc	gcg	2492
209	Ile	Pro	Phe	Leu	Glu	His	Asp	Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Ala	
210									585			590				595	
212	aac	atg	cag	aag	cag	gct	gtg	cca	ctg	att	cgt	gcc	gag	gct	cct	ttc	2540
213	Asn	Met	Gln	Lys	Gln	Ala	Val	Pro	Leu	Ile	Arg	Ala	Glu	Ala	Pro	Phe	
214									600			605				610	
216	gtg	ggc	acc	ggt	atg	gag	cag	cgc	gca	gca	tac	gac	gcc	ggc	gac	ctg	2588
217	Val	Gly	Thr	Gly	Met	Glu	Gln	Arg	Ala	Ala	Tyr	Asp	Ala	Gly	Asp	Leu	
218									615			620				625	
220	gtt	att	acc	cca	gtc	gca	ggt	gtg	gtg	gaa	aac	gtt	tca	gct	gac	ttc	2636
221	Val	Ile	Thr	Pro	Val	Ala	Gly	Val	Val	Glu	Asn	Val	Ser	Ala	Asp	Phe	
222									630			635				640	645
224	atc	acc	atc	atg	gtc	gat	gac	ggc	aag	cgc	gaa	acc	tac	ctg	ctg	cgt	2684
225	Ile	Thr	Ile	Met	Ala	Asp	Asp	Gly	Lys	Arg	Glu	Thr	Tyr	Leu	Leu	Arg	
226									650			655				660	
228	aag	ttc	cag	cgc	acc	aac	cag	ggc	acc	agc	tac	aac	cag	aag	cct	ttg	2732
229	Lys	Phe	Gln	Arg	Thr	Asn	Gln	Gly	Thr	Ser	Tyr	Asn	Gln	Lys	Pro	Leu	
230									665			670				675	
232	gtt	aac	ttg	ggc	gag	cgc	gtt	gaa	gct	ggc	cag	gtt	att	gct	gat	ggt	2780
233	Val	Asn	Leu	Gly	Glu	Arg	Val	Glu	Ala	Gly	Gln	Val	Ile	Ala	Asp	Gly	
234									680			685				690	
236	cca	ggt	acc	ttc	aat	ggt	gaa	atg	tcc	ctt	ggc	cgt	aac	ctt	ctg	gtt	2828
237	Pro	Gly	Thr	Phe	Asn	Gly	Glu	Met	Ser	Leu	Gly	Arg	Asn	Leu	Leu	Val	
238									695			700				705	
240	gcg	ttc	atg	cct	tgg	gaa	ggc	cac	aac	tac	gag	gat	gcg	atc	atc	ctc	2876
241	Ala	Phe	Met	Pro	Trp	Glu	Gly	His	Asn	Tyr	Glu	Asp	Ala	Ile	Ile	Leu	
242									710			715				720	725
244	aac	cag	aac	atc	gtt	gag	cag	gac	atc	ttg	acc	tcg	atc	cac	atc	gag	2924
245	Asn	Gln	Asn	Ile	Val	Glu	Gln	Asp	Ile	Leu	Thr	Ser	Ile	His	Ile	Glu	
246									730			735				740	
248	gag	cac	gag	atc	gtt	gac	act	aag	ctt	ggc	gcc	gaa	gaa	atc			2972
249	Glu	His	Glu	Ile	Asp	Ala	Arg	Asp	Thr	Lys	Leu	Gly	Ala	Glu	Glu	Ile	
250									745			750				755	
252	acc	cgc	gac	atc	cct	aat	gtg	tct	gaa	gaa	gtc	ctc	aag	gac	ctc	gac	3020
253	Thr	Arg	Asp	Ile	Pro	Asn	Val	Ser	Glu	Glu	Val	Leu	Lys	Asp	Leu	Asp	
254									760			765				770	
256	gac	cgc	ggt	att	gtc	cgc	atc	ggt	gct	gat	gtt	cgt	gac	ggc	gac	atc	3068
257	Asp	Arg	Gly	Ile	Val	Arg	Ile	Gly	Ala	Asp	Val	Arg	Asp	Gly	Asp	Ile	
258									775			780				785	
260	ctg	gtc	ggt	aag	gtc	acc	cct	aag	ggc	gag	acc	gag	ctc	acc	ccg	gaa	3116
261	Leu	Val	Gly	Lys	Val	Thr	Pro	Lys	Gly	Glu	Thr	Glu	Leu	Thr	Pro	Glu	
262									790			795				800	805
264	gag	cgc	ttg	ctg	cgc	gca	atc	ttc	ggt	gag	aag	gcc	cgc	gaa	gtt	cgc	3164
265	Glu	Arg	Leu	Leu	Arg	Ala	Ile	Phe	Gly	Glu	Lys	Ala	Arg	Glu	Val	Arg	

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268	gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc			3212
269	Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly			
270	825	830	835	
272	gtg cgt cac ttc tcc cgc gag gac gac gat ctg gct cct ggc gtc			3260
273	Val Arg His Phe Ser Arg Glu Asp Asp Asp Leu Ala Pro Gly Val			
274	840	845	850	
276	aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac			3308
277	Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp			
278	855	860	865	
280	ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa			3356
281	Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys			
282	870	875	880	885
284	att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt			3404
285	Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val			
286	890	895	900	
288	gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt			3452
289	Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly			
290	905	910	915	
292	cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc			3500
293	Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser			
294	920	925	930	
296	gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct			3548
297	Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro			
298	935	940	945	
300	gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg			3596
301	Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val			
302	950	955	960	965
304	tcc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca			3644
305	Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser			
306	970	975	980	
308	cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca			3692
309	Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala			
310	985	990	995	
312	acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt			3737
313	Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val			
314	1000	1005	1010	
316	tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac			3782
317	Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp			
318	1015	1020	1025	
320	gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc			3827
321	Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr			
322	1030	1035	1040	
324	cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc			3872
325	Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe			
326	1045	1050	1055	
328	ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac			3917
329	Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr			
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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number